In the Claims:

Please cancel claims 2, 10, 16, 17, 25, 27, 29 and 30 without prejudice.
The claims, including amendments, should now read as follows:

1. (Currently Amended) A process for ~~detecting~~ determining a single nucleotide polymorphism (SNP) in a target polynucleotide using no ligation step comprising:

(a) contacting one or more allele specific oligonucleotide primers (P1) with one or more target polynucleotides (TP), wherein said target polynucleotide possesses a first portion that is complementary to a second portion located on said P1 at or near one end ~~thereof~~ of said P1 but wherein the terminal nucleotide, and third nucleotide from the terminal nucleotide, at said end of said P1 may independently not be complementary to the corresponding nucleotide of said target polynucleotide, and wherein such contacting occurs under conditions that promote hybridization between ~~the~~ said first and second portions thereby forming ~~an~~ a P1-TP complex;

(b) contacting the P1-TP complex of (a) with an exonuclease deficient deoxyribonucleotide (DNA) polymerase enzyme under conditions that promote extension of the P1 with the TP as template when the terminal nucleotide at the end of said P1 is complementary to the corresponding nucleotide of said target polynucleotide thereby forming an extended segment (ES) of P1;

(c) ~~detecting~~ determining the extended P1 by removing the target polynucleotide from the complex formed in step (b) and contacting a primer oligonucleotide (P2) with the extended P1, wherein P2 comprises a portion that hybridizes to the extended segment of P1 and not to the non-extended portion of P1 and under conditions promoting such hybridization; ~~and~~

(d) ~~detecting~~ determining said hybridization of P2 and extended P1 by contacting an amplification target circle (ATC) with said hybridized P2 and extended P1 wherein said P2 comprises a first portion that hybridizes to the extended segment of P1 and not to the non-extended portion of P1 and a second portion that hybridizes to said ATC but not to P1, wherein P2 is a primer that supports rolling circle amplification, and under conditions promoting hybridization of the ATC to P2 to form hybridized ATC-P2;

(e) contacting said hybridized ATC-P2 with a DNA polymerase under conditions promoting extension of P2 to produce rolling circle amplification of said ATC and thereby generating tandem sequence DNA (TS-DNA); and

(f) determining production of said TS-DNA thereby determining hybridization of P2 with extended P1

whereby ~~said hybridization indicates extension of P1 thereby detecting an SNP in the target polynucleotide~~ production of said TS-DNA determines an SNP in said TP.

2. (Canceled)

3. (Currently Amended) The process of claim ~~2~~ 1 wherein P2 comprises two 3'-ends.

4. (Currently Amended) The process of claim ~~2~~ 1 wherein the target polynucleotide is derived from genomic DNA.

5. (Original) The process of claim 4 wherein the genomic DNA is human genomic DNA.

6. (Original) The process of claim 4 wherein the genomic DNA is non-human genomic DNA.

7. (Previously Amended) The process of claim 4 wherein the target polynucleotide is a mixture of human and non-human genomic DNA.

8. (Currently Amended) The process of claim ~~2~~ 1 wherein the DNA polymerase of step (b) is an enzyme selected from the group consisting of bacteriophage φ29 DNA polymerase, phage M2 DNA polymerase, phage φ-PRD1 DNA polymerase, VENT® DNA polymerase, Klenow fragment of DNA polymerase I, T5 DNA polymerase, PRD1 DNA polymerase, T4 DNA polymerase, *E. coli* DNA polymerase III holoenzyme, Tts polymerase and T7 DNA polymerase.

9. (Original) The process of claim 1 wherein the exonuclease-deficient DNA polymerase is T7 Sequenase or Tth polymerase.

10. (Canceled)

11. (Currently Amended) The process of claim ~~10~~ 1 wherein the DNA polymerase of step (e) is an enzyme selected from the group consisting of Klenow polymerase (exo$^-$), Vent polymerase (exo$^-$), Deep Vent polymerase (exo$^-$), Pfu polymerase (exo$^-$), Taq polymerase, the Stoeffel fragment of Taq polymerase, Bst polymerase, Tts polymerase, and ThermoSequenase.

12. (Original) The process of claim 1 wherein at least one end of the allele specific oligonucleotide primers (P1) is attached to a solid support.

13. (Original) The process of claim 12 wherein the solid support is composed of at least one member selected from the group consisting of acrylamide, cellulose,

nitrocellulose, glass, polystyrene, polyethylene vinyl acetate, polypropylene, polymethacrylate, polyethylene, polyethylene oxide, glass, polysilicates, polycarbonates, teflon, fluorocarbons, nylon, silicon rubber, polyanhydrides, polyglycolic acid, polylactic acid, polyorthoesters, polypropylfumerate, collagen, glycosaminoglycans, and polyamino acids.

14. (Original) The process of claim 12 wherein said solid support is made of glass or plastic.

15. (Original) The process of claim 1 wherein the allele specific oligonucleotide primer (P1) is selected from the group consisting of the sequences of SEQ ID NOs: 1, 2, 3, 4, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, and 26.

16. (Canceled)

17. (Canceled)

18. (Currently Amended) A method for diagnosing a disease characterized by a ~~genetic mutation~~ mutated gene sequence comprising:

(a) obtaining a sample of a mutated gene sequence from an organism afflicted with said disease; and

(b) carrying out the process of claim 1 wherein at least a portion of said mutated gene sequence is used as either the target polynucleotide or the allele specific oligonucleotide.

19. (Original) The process of claim 18 wherein the mutated gene sequence is used as the target polynucleotide.

20. (Original) The process of claim 18 wherein said animal is a human.

21. (Original) The process of claim 18 wherein said disease is a disease caused by, induced by or related to a mutation in at least one gene.

22. (Original) The process of claim 21 wherein said disease is a member selected from the group consisting of Parlinson's disease, Duchenne muscular dystrophy, Niemann-Pick disease, polyposis, neurofibromatosis, polycystic kidney disease, Tay-Sachs disease, xeroderma pigmentosa, ataxia-telangiectasia, Huntington disease, Li-Fraumeni syndrome, beta-thalassemia, sickle cell anemia, hemoglobin C disease, hemophilia, acute intermittent porphyria, cystic fibrosis, diabetes, obesity and cancer.

23. (Original) The process of claim 22 wherein said cancer is a member selected from the group consisting of leukemia, lymphoma, melanoma, neuroblastoma, retinoblastoma, rhabdomyosarcoma, Ewing sarcoma, head and neck cancer, skin cancer, brain cancer, esophageal cancer, stomach cancer, lung cancer, breast cancer, colon cancer, ovarian cancer, testicular cancer and prostate cancer.

24. (Original) The process of claim 1 wherein the third nucleotide from the end of said P1 is complementary to the corresponding nucleotide of the target polynucleotide.

25. (Canceled)

26. (Original) The process of claim 1 wherein the third nucleotide from the end of said P1 is not complementary to the corresponding nucleotide of the target polynucleotide.

27. (Canceled)

28. (Original) The process of claim 1 wherein each of the terminal nucleotide and third nucleotide from the end of said P1 is not complementary to the corresponding nucleotide of the target polynucleotide.

29. (Canceled)

30. (Canceled)

31. (Previously Added) A process for detecting a single nucleotide polymorphism (SNP) in a target polynucleotide, comprising:

(a) contacting one or more allele specific oligonucleotide primers (P1) with one or more target polynucleotides (TP), wherein said target polynucleotide possesses a first portion that is complementary to a second portion located on said P1 at or near one end thereof but wherein the terminal nucleotide, and third nucleotide from the terminal nucleotide, at said end of said P1 may not be complementary to the corresponding nucleotide of said target polynucleotide, and wherein such contacting occurs under conditions that promote hybridization between the first and second portions thereby forming an P1-TP complex and wherein P1 comprises the nucleotide sequence of SEQ ID NO: 13;

(b) contacting the P1-TP complex of (a) with an exonuclease deficient deoxyribonucleotide (DNA) polymerase enzyme under conditions that promote extension of the P1 with the TP as template thereby forming an extended segment (ES) of P1; and

(c) detecting the extended P1

thereby detecting an SNP in said target polynucleotide.